STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/520,033_
Source: _PCT/10_
Date Processed by STIC: _1/10/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: _10/520,033_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2___Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
Numbering   use **space characters**, instead.

4_____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
is Artificial Sequence

11_____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033   TIME: 08:16:21

        Input Set : A:\PTO.DA.txt
        Output Set: N:\CRF4\01102006\J520033.raw   *see item 2 on Error Summary Sheet*

   3 <110> APPLICANT: Chan, Raquel
   5 <120> TITLE OF INVENTION: Transcription factor gene induced by water deficit conditions and
   6   abscisic acid from Helianthus annuus, promoter and transgenic plants   *these lines exceed 72 characters*
   8 <130> FILE REFERENCE: US PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/520,033
C--> 10 <141> CURRENT FILING DATE: 2004-12-30
  10 <160> NUMBER OF SEQ ID NOS: 22
  12 <170> SOFTWARE: PatentIn version 3.1   *see pp 1-6*

ERRORED SEQUENCES   *delete all alphabetical headings*   *Does Not Comply Corrected Diskette Needed*

E--> 14 <210>   SEQ ID NO.1   *1 <-- just show "1"*
  15 <211> LENGTH: 774   *do NOT use alphabetical headings in a "new" sequence*
  16 <212> TYPE: DNA
  17 <213> ORGANISM: Helianthus annuus   *Rules format sequence listing*
  19 <400> SEQUENCE: 1
  20 tcactagtac cataatattc acaaacacac acacctcaga aacgaagctt gcacataatg   60
  22 tctcttcaac aagtacccac aacagaaaca accaccagga agaaccgaaa cgaggggcgg   120
  24 aaacgattta ccgacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga   180
  26 cccgagttaa ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg   240
  28 gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat   300
  30 aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtctct aaagaaagag   360
  32 aatcaggccc tactcaatca ggtatggttg caaacttaca atgttgcatt caactatttca   420
  34 agtagttttg aatttttgtg acaataaaga ttgacaaatg ttgtttgata attgattaac   480
  36 agttggaggt gctgagaaat gtagcagaaa agcatcaaga gaaaactagt agtagtggca   540
  38 gcggtgaaga atcggatgat cggtttacga actctccgga cgttatgttt ggtcaagaaa   600
  40 tgaatgttcc gttttgcgac ggtttttgcgt actttgaaga aggaaacagt ttgttggaga   660
  42 ttgaagaaca actgccagac cctcaaaagt ggtgggagtt ctaaagagta aagaaggatg   720
  44 tagaagtagt agagtaaaaa ctaaaacata ccagatagtt ggtttacact ttgt   774
E--> 47 <210>   SEQ ID NO. 2
  48 <211> LENGTH: 673
  49 <212> TYPE: DNA
  50 <213> ORGANISM: Helianthus annuus
  52 <400> SEQUENCE: 2
  53 tcactagtac cataatattc acaaacacac acacctcaga aacgaagctt gcacataatg   60
  55 tctcttcaac aagtacccac aacagaaaca accaccagga agaaccgaaa cgaggggcgg   120
  57 aaacgattta ccgacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga   180
  59 cccgagttaa ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg   240
  61 gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat   300
  63 aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtctct aaagaaagag   360
  65 aatcaggccc tactcaatca gttggaggtg ctgagaaatg tagcagaaaa gcatcaagag   420
  67 aaaactagta gtagtggcag cggtgaagaa tcggatgatc ggtttacgaa ctctccggac   480

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/520,033

DATE: 01/10/2006
TIME: 08:16:21

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

```
 69 gttatgtttg gtcaagaaat gaatgttccg ttttgcgacg gttttgcgta ctttgaagaa      540
 71 ggaaacagtt tgttggagat tgaagaacaa ctgccagacc ctcaaaagtg gtgggagttc      600
 73 taaagagtaa agaaggatgt agaagtagta gagtaaaaac taaaacatac cagatagttg      660
 75 gtttacactt tgt                                                         673
```
E--> 78 <210>   SEQ ID NO 3
```
 79 <211> LENGTH: 1221
 80 <212> TYPE: DNA
 81 <213> ORGANISM: Helianthus annuus
 83 <220> FEATURE:
 84 <221> NAME/KEY: promoter
 85 <222> LOCATION: (1)..(1221)
 86 <223> OTHER INFORMATION: Large allele
```
89 <400> SEQUENCE: 3
```
 90 gatccaattg gaccacctgg cacatcgtat cttatctctt ttgtcgtttc caacacacca       60
 92 caacacacct acaaacgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc      120
 94 atattaaaag tagtagcccc cacccccatt tgttacctac catttcccac tttaataatc      180
 96 acccacgcta tgtccacttg tacttttgtt tgcacacaac tcttcccata aaatatcaaa      240
 98 ccaaattttt tttagtggaa aacaaattcc ccaaatagaa tactaacgaa attcatcgca      300
100 tcagaataca ctcatctctg aacagtggcg aagcttgacg ttttcgacgg ggggtcggaa      360
102 aacgtatgta cccgaaattt ctatagaatc ggggggtcga aaacgtatat acccaaaatt      420
104 tctatacgaa aactacatat ataacactac tgagcaaaaa gttcgggggt tcgggcgccc      480
106 ctccggcccc cttcaaagct tcgccaatgt ctctgaaccg aagaaaaccc tcactcgtct      540
108 actagccaat gaatcctcac caggaaaacc ctcactcgtc ttactggact attggcgctt      600
110 ccaaatggac tacttgcgaa attcaccaca tcgggataca ctcgtctact gcggtgaggt      660
112 aaaacccgct tggctcaagg atcgaactag cgattgctgc ctactcgcct aatctcccat      720
114 catcaacagg tgccgccgaa acaaaatgct ggggcggga gttgaaccta ggtccagtga      780
116 cgcacccatg aattttttt ctagggatgc gaacgagtgg tttaaccata ctttaagag      840
118 gtgcgatcgg aaattttacc tataaaatac actaaaaaag ttccaagggt ccacccaccc      900
120 cttaacctaa gtccgccttt gtctggatca cgtgaaacat caggtctctc ccttaccagt      960
122 ccagctacga ctcattgaca aaatatcaaa accatatgat tttgagtttt atctcaaccg     1020
124 aaagtgacat catgacagag aatcgacata accaaaacgt gtaaacgtac aactcaccat     1080
126 tgcgttgaaa aggacaaaac aggtaggatt cttgtcaaat tcaacgcgta cacctgtgct     1140
128 tcatctaaac cccatacttt aagaaccttt ataaagacca ctcactatat atacacatat     1200
130 ataatatcac ttatcaaacc c                                               1221
```
E--> 133 <210>   SEQ ID NO 4
```
134 <211> LENGTH: 28
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Hind I
140       II site
```
142 <400> SEQUENCE: 4
```
143 gcgaagcttg atgcgaacga gtggttta                                          28
```
E--> 146 <210>   SEQ ID NO 5
```
147 <211> LENGTH: 28
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Sal I
```

RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033   TIME: 08:16:21

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J520033.raw**

```
      153      site
  155 <400> SEQUENCE: 5
  156 gcggtcgaca cctggcacat cgtatctt                                            28
E--> 159 <210> :           SEQ ID NO. 6
  160 <211> LENGTH: 27
  161 <212> TYPE: DNA
  162 <213> ORGANISM: Artificial
  164 <220> FEATURE:
  165 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Bam HI
  166      site
  168 <400> SEQUENCE: 6
  169 cgcggatccg agggtttgat aagtgat                                             27
E--> 172 <210>           SEQ ID NO. 7
  173 <211> LENGTH: 27
  174 <212> TYPE: DNA
  175 <213> ORGANISM: Artificial
  177 <220> FEATURE:
  178 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Hind I
  179      II site
  181 <400> SEQUENCE: 7
  182 cccaagctta acctaagtcc gcctttg                                             27
E--> 185 <210>           SEQ ID NO. 8
  186 <211> LENGTH: 27
  187 <212> TYPE: DNA
  188 <213> ORGANISM: Artificial
  190 <220> FEATURE:
  191 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Hind II
  192      I site
  194 <400> SEQUENCE: 8
  195 ggcaagctta tctcaaccga aagtgac                                             27
E--> 198 <210>           SEQ ID NO. 9
  199 <211> LENGTH: 19
  200 <212> TYPE: DNA
  201 <213> ORGANISM: Artificial
  203 <220> FEATURE:
  204 <223> OTHER INFORMATION: Designed oligonucleotide based on the 5' promoter
  206 <400> SEQUENCE: 9
  207 atttcgcaag tagtccatt                                                      19
E--> 210 <210>           SEQ ID NO. 10
  211 <211> LENGTH: 1015
  212 <212> TYPE: DNA
  213 <213> ORGANISM: Helianthus annuus
  215 <400> SEQUENCE: 10
  216 gatccaattg gaccacctgg cacatcgtat cttatctctt ttgtcgtttc caacacacca       60
  218 caacacacct acaaacgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc      120
  220 atattaaaag tagtagcccc caccccatt tgttacctac catttcccac tttaataatc      180
  222 acccacgcta tgtccacttg tacttttgtt tgcacacaac tcttcccata aaatatcaaa      240
  224 ccaaattttt tttaatggaa aacaaatact tcaaatgcac tattggtgaa attcaccaca      300
  226 tcagaataca cccgtctcta ctcatctact ggccaacgaa tcttcacggg ggaaaccctc      360
```

RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033   TIME: 08:16:21

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J520033.raw**

```
228 actcgtctac tgggactact ggcgcttcaa aatggactac tgacaaaatt caccacatcg   420
230 ggatacactt gtctactgcg gtgaggtaaa atccgccgct cagctcaatg atcgaactag   480
232 cgatcgccac ccactcacct tgtctcccat catcaccagg tgccgccaaa acaaaatgtt   540
234 gggggcggga attgaaccta ggtccagtgg cgcacccatg aatttttttt ctagggatgc   600
236 gaacgagtga tttaaccata cttttaagag gtgcgatcgg aaattttacc tataaaatat   660
238 actaaaaaaa tttcaagggt ccgcccaccc acccccttaac ctaagtccgc ctctgcctgg   720
240 atcacgtgaa acatcaggtc tctctcttac cagttcacct acaactcatt gacaaaatat   780
242 caaaaccata tgattttgag ttttatctca accgaaagtg acatcatgac agagaatcga   840
244 cataaccaaa acgtgtaaac gtacaactca ccattgcgtt gaaaaggaca aaacaggtag   900
246 gattcttgtc aaattcaacg cgtacacctg tgcttcatct aaaccccata ctttaagaac   960
248 ctttataaag accactcact atatatacac atatataata tcacttatca aaccc       1015
```
E--> 251 <210> .   SEQ ID NO. 11
    252 <211> LENGTH: 28
    253 <212> TYPE: DNA
    254 <213> ORGANISM: Artificial
    256 <220> FEATURE:
    257 <223> OTHER INFORMATION: Designed oligonucleotide that matches nucleotides 81-100 of
the H
    258   ahb-4 cDNA sequence and having Bam HI site
E--> 260 <400> SEQUENCE: 11
    261 ggcggatcca acagaaacaa ccaccagg   28
E--> 264 <210>   SEQ ID NO. 12
    265 <211> LENGTH: 29
    266 <212> TYPE: DNA
    267 <213> ORGANISM: Artificial
    269 <220> FEATURE:
    270 <223> OTHER INFORMATION: Designed oligonucleotide for cloning 5' cDNA and having Bam
HI s
    271   ite
E--> 273 <400> SEQUENCE: 12
    274 ggcggatccc ctggtggttg tttctgttg   29
E--> 277 <210>   SEQ ID NO. 13
    278 <211> LENGTH: 34
    279 <212> TYPE: DNA
    280 <213> ORGANISM: Artificial
    282 <220> FEATURE:
    283 <223> OTHER INFORMATION: oligonucleotide based on 5' cDNA and having Xho I site
E--> 285 <400> SEQUENCE: 13
    286 gaggactcga gctcaagttt tttttttttt tttt   34
E--> 289 <210>   SEQ ID NO. 14
    290 <211> LENGTH: 18
    291 <212> TYPE: DNA
    292 <213> ORGANISM: Artificial
    294 <220> FEATURE:
    295 <223> OTHER INFORMATION: Oligonucleotide based on 5' cDNA and having Xho I site
E--> 297 <400> SEQUENCE: 14
    298 gaggactcga gctcaagc   18
E--> 301 <210> :   . SEQ ID NO. 15
    302 <211> LENGTH: 29
    303 <212> TYPE: DNA
    304 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033 TIME: 08:16:21

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J520033.raw**

```
       306 <220> FEATURE:
       307 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Eco RI
       308      site
       310 <400> SEQUENCE: 15
       311 gccgaattca gattgagcaa gagtataac                                    29
E--> 314 <210>              SEQ ID NO.16
       315 <211> LENGTH: 19
       316 <212> TYPE: DNA
       317 <213> ORGANISM: Artificial
       319 <220> FEATURE:
       320 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter
       322 <400> SEQUENCE: 16
       323 acctttataa agaccactc                                              19
E--> 326 <210>              SEQ ID NO.17
       327 <211> LENGTH: 19
       328 <212> TYPE: DNA
       329 <213> ORGANISM: Artificial
       331 <220> FEATURE:
       332 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter
       334 <400> SEQUENCE: 17
       335 acgcaatggt gagttgtac                                              19
E--> 338 <210>              SEQ ID NO.18
       339 <211> LENGTH: 24
       340 <212> TYPE: DNA
       341 <213> ORGANISM: Artificial
       343 <220> FEATURE:
       344 <223> OTHER INFORMATION: oligonucleotide to DNA-binding assays
       346 <400> SEQUENCE: 18
       347 aattcagatc tcaataattg agag                                        24
E--> 350 <210>              SEQ ID NO.19
       351 <211> LENGTH: 24
       352 <212> TYPE: DNA
       353 <213> ORGANISM: Artificial
       355 <220> FEATURE:
       356 <223> OTHER INFORMATION: oligonucleotide to DNA-binding assays
       358 <400> SEQUENCE: 19
       359 gatcctctca attattgaga tctg                                        24
E--> 362 <210>              SEQ ID NO.20
       363 <211> LENGTH: 30
       364 <212> TYPE: DNA
       365 <213> ORGANISM: Artificial
       367 <220> FEATURE:
       368 <223> OTHER INFORMATION: Oligonucleotide having Bam HI site
       370 <400> SEQUENCE: 20
       371 gcgggatcca ccatgtctct tcaacaagta                                  30
E--> 374 <210>              SEQ ID NO.21
       375 <211> LENGTH: 30
       376 <212> TYPE: DNA
       377 <213> ORGANISM: Artificial
```

RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033   TIME: 08:16:21

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J520033.raw**

```
379 <220> FEATURE:
380 <223> OTHER INFORMATION: Oligonucleotide having Sac I site
382 <400> SEQUENCE: 21
383 gccgagctct tagaactcca accacttttg                                30
386 <210>          SEQ ID NO.22
387 <211> LENGTH: 27
388 <212> TYPE: DNA
389 <213> ORGANISM: Artificial
391 <220> FEATURE:
392 <223> OTHER INFORMATION: Oligonucleotide having Bam HI site
394 <400> SEQUENCE: 22
395 ggcggatccg tctcccagtt gttcttc                                  27
398 7
```

delete

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J520033.raw**

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:19 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
L:47 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:52 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2
L:78 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:89 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:3
L:133 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:142 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:4
L:146 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:155 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:5
L:159 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:168 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:6
L:172 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:181 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:7
L:185 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:194 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:8
L:198 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:206 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:9
L:210 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:215 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:10
L:251 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:260 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:11
L:264 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:273 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:12
L:277 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:285 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:13
L:289 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:297 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:14
L:301 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:15
L:314 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:322 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:16
L:326 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:334 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:17
L:338 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:346 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:18
L:350 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:358 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:19
L:362 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:370 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:20
L:374 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:21
L:386 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:394 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:22
L:398 M:254 E: No. of Bases conflict, this line has no nucleotides.
```